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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=6; day=19; hr=15; min=15; sec=19; ms=314;]

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Reviewer Comments:

<210> 23

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> PP2A motif

<400> 23

Gly Asp Xaa His Gln Gly Gln

1 5

A mandatory feature is required to cover every "Xaa" used in a sequence. SEQ ID # 23 and 24 does not have a feature to cover the "Xaa" at positions 3, and 3,5. Please check for similar errors and make all necessary changes.

Application No: 10590551 Version No: 2.0

Input Set:**Output Set:**

Started: 2009-06-03 19:00:30.722
Finished: 2009-06-03 19:00:33.549
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 827 ms
Total Warnings: 15
Total Errors: 5
No. of SeqIDs Defined: 26
Actual SeqID Count: 26

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
E 341	'Xaa' position not defined SEQID (23) POS (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
E 341	'Xaa' position not defined SEQID (24) POS (3)
E 341	'Xaa' position not defined SEQID (24) POS (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)

SEQUENCE LISTING

<110> Genomine, Inc.
POSTECH FOUNDATION

<120> Novel Phytochrome-interacting protein and a use thereof

<130> OP05-1002

<140> 10590551
<141> 2009-06-03

<150> KR10-2004-0013663
<151> 2004-02-27

<160> 26

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<213> Artificial Sequence

<220>
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<210> 2
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<212> DNA
<213> Artificial Sequence

<220>
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ctcgagctac ttgttgctg cagcgagttc 30

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<211> 1455
<212> DNA
<213> Arabidopsis thaliana

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gaactcaaca gcaacaacgc tggatgttgg gcaaatcggtt catttgctca cacaactg 180

gaggaaatatg gcagtgaat acaggatgca tcgaaggcca ttgaagttga ttcaagatac 240
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caatattctg gtgctagaat tgagggagag gaagttacct tagattttgt gaaaacgatg 540
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<213>	Arabidopsis thaliana

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Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
35 40 45

Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
50 55 60

Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
65 70 75 80

Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
85 90 95

Phe Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Arg Leu Ser Pro
100 105 110

Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
115 120 125

Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
130 135 140

Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
145 150 155 160

Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
165 170 175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
180 185 190

Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
195 200 205

Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
210 215 220

Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
225 230 235 240

Glu Leu Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
245 250 255

Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
260 265 270

Phe Ala Phe Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
275 280 285

Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
290 295 300

Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
305 310 315 320

Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
325 330 335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
340 345 350

Arg Ala Ile Asp Arg Phe Cys Glu Pro Pro Glu Glu Gly Leu Met Cys
355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
420 425 430

Ser Ala Pro Asn Tyr Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile
435 440 445

Arg Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala
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Val Pro His Pro Asp Val Lys Pro Met Ala Tyr Ala Asn Asn Phe Leu
465 470 475 480

Arg Met Phe Asn

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<220>
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<210> 6
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<213> Artificial Sequence

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<223> PCR primer

<400> 6
ctcgagttag ttgaacatcc tgag 24

<210> 7
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<220>
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<400> 7
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28

<210> 8
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<212> DNA
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<400> 8
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34

<210> 9
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34

<210> 10
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27

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

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<220>
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<400>      11
ggatccatgc cagtatctga aaggcgt

<210>      12
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<212>      DNA
<213>      Artificial Sequence

<220>
<223>      PCR primer

<400>      12
atggagacca agaatgagaa ttct

<210>      13
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ttagttgaac atcctgagaa agtt

<210>      14
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<212>      PRT
<213>      Arabidopsis thaliana

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 20          25           30

Glu Glu Val Thr Leu Asp Phe Val Lys Thr Met Met Glu Asp Phe Lys
 35          40           45

Asn Gln Lys Thr Leu His Lys Arg Tyr Ala Tyr Gln Ile Val Leu Gln
 50          55           60

Thr Arg Gln Ile Leu Leu Ala Leu Pro Ser Leu Val Asp Ile Ser Val
 65          70           75           80

Pro His Gly Lys His Ile Thr Val Cys Gly Asp Val His Gly Gln Phe

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27

24

85

90

95

Tyr Asp Leu Leu Asn Ile Phe Glu Leu Asn Gly Leu Pro Ser Glu Glu
 100 105 110

Asn Pro Tyr Leu Phe Asn Gly Asp Phe Val Asp Arg Gly Ser Phe Ser
 115 120 125

Val Glu Ile Ile Leu Thr Leu Phe Ala Phe Lys Cys Met Cys Pro Ser
 130 135 140

Ser Ile Tyr Leu Ala Arg Gly Asn His Glu Ser Lys Ser Met Asn Lys
 145 150 155 160

Ile Tyr Gly Phe Glu Gly Glu Val Arg Ser Lys Leu Ser Glu Lys Phe
 165 170 175

Val Asp Leu Phe Ala Glu Val Phe Cys Tyr Leu Pro Leu Ala His Val
 180 185 190

Ile Asn Gly Lys Val Phe Val Val His Gly Gly Leu Phe Ser Val Asp
 195 200 205

Gly Val Lys Leu Ser Asp Ile Arg Ala Ile Asp Arg Phe Cys Glu Pro
 210 215 220

Pro Glu Glu Gly Leu Met Cys Glu Leu Leu Trp Ser Asp Pro Gln Pro
 225 230 235 240

Leu Pro Gly Arg Gly Pro Ser Lys Arg Gly Val Gly Leu Ser Phe Gly
 245 250 255

Gly Asp Val Thr Lys Arg Phe Leu Gln Asp Asn Asn Leu Asp Leu Leu
 260 265 270

Val Arg Ser His Glu Val Lys Asp Glu Gly Tyr Glu Val Glu His Asp
 275 280 285

Gly Lys Leu Ile Thr Val Phe Ser Ala Pro Asn Tyr Cys Asp Gln Met
 290 295 300

Gly Asn Lys Gly Ala Phe Ile Arg Phe Glu Ala Pro Asp Met Lys Pro
 305 310 315 320

Asn Ile Val Thr Phe Ser Ala Val Pro His Pro Asp Val Lys Pro Met
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Ala Tyr Ala Asn Asn Phe Leu Arg Met Phe Asn
 340 345

<210> 15
 <211> 1041
 <212> DNA
 <213> Arabidopsis thaliana

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acgatgatgg	aggatttaa	gaaccaaaaa	acattgcata	aacggtatgc	ctatcaaatc	180
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 <213> Homo sapiens

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 20 25 30

Ile Asp Leu Tyr Thr Lys Ala Ile Glu Leu Asn Ser Asn Asn Ala Val
 35 40 45

Tyr Trp Ala Asn Arg Ala Phe Ala His Thr Lys Leu Glu Glu Tyr Gly
50 55 60

Ser Ala Ile Gln Asp Ala Ser Lys Ala Ile Glu Val Asp Ser Arg Tyr
65 70 75 80

Ser Lys Gly Tyr Tyr Arg Arg Gly Ala Ala Tyr Leu Ala Met Gly Lys
85 90 95

Glu Lys Asp Ala Leu Lys Asp Phe Gln Gln Val Lys Gly Leu Ser Pro
100 105 110

Asn Asp Pro Asp Ala Thr Arg Lys Leu Lys Glu Cys Glu Lys Ala Val
115 120 125

Met Lys Leu Lys Phe Glu Glu Ala Ile Ser Val Pro Val Ser Glu Arg
130 135 140

Arg Ser Val Ala Glu Ser Ile Asp Phe His Thr Ile Glu Val Glu Pro
145 150 155 160

Gln Tyr Ser Gly Ala Arg Ile Glu Gly Glu Glu Val Thr Leu Asp Phe
165 170 175

Val Lys Thr Met Met Glu Asp Phe Lys Asn Gln Lys Thr Leu His Lys
180 185 190

Arg Tyr Ala Tyr Gln Ile Val Leu Gln Thr Arg Gln Ile Leu Leu Ala
195 200 205

Leu Pro Ser Leu Val Asp Ile Ser Val Pro His Gly Lys His Ile Thr
210 215 220

Val Cys Gly Asp Val His Gly Gln Phe Tyr Asp Leu Leu Asn Ile Phe
225 230 235 240

Glu Asp Asn Gly Leu Pro Ser Glu Glu Asn Pro Tyr Leu Phe Asn Gly
245 250 255

Asp Phe Val Asp Arg Gly Ser Phe Ser Val Glu Ile Ile Leu Thr Leu
260 265 270

Phe Ala Glu Lys Cys Met Cys Pro Ser Ser Ile Tyr Leu Ala Arg Gly
275 280 285

Asn His Glu Ser Lys Ser Met Asn Lys Ile Tyr Gly Phe Glu Gly Glu
290 295 300

Val Arg Ser Lys Leu Ser Glu Lys Phe Val Asp Leu Phe Ala Glu Val
305 310 315 320

Phe Cys Tyr Leu Pro Leu Ala His Val Ile Asn Gly Lys Val Phe Val
325 330 335

Val His Gly Gly Leu Phe Ser Val Asp Gly Val Lys Leu Ser Asp Ile
340 345 350

Arg Ala Ile Asp Arg Phe Cys Glu Pro Phe Glu Glu Gly Leu Met Cys
355 360 365

Glu Leu Leu Trp Ser Asp Pro Gln Pro Leu Pro Gly Arg Gly Pro Ser
370 375 380

Lys Arg Gly Val Gly Leu Ser Phe Gly Gly Asp Val Thr Lys Arg Phe
385 390 395 400

Leu Gln Asp Asn Asn Leu Asp Leu Leu Val Arg Ser His Glu Val Lys
405 410 415

Asp Glu Gly Tyr Glu Val Glu His Asp Gly Lys Leu Ile Thr Val Phe
420 425 430

Ser Ala Pro Asn Cys Asp Gln Met Gly Asn Lys Gly Ala Phe Ile Arg
435 440 445

Phe Glu Ala Pro Asp Met Lys Pro Asn Ile Val Thr Phe Ser Ala Val
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Pro His Pro Met Ala Tyr Ala Asn Asn Phe Ile Arg Met Phe Asn
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<210> 17
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<213> Homo sapiens

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20 25 30

Phe Lys Ala Lys Asp Tyr Glu Asn Ala Ile Lys Phe Tyr Ser Gln Ala
35 40 45

Ile Glu Leu Asn Pro Ser Asn Ala Ile Tyr Tyr Gly Asn Arg Ser Leu
50 55 60

Ala Tyr Leu Arg Thr Glu Cys Tyr Gly Tyr Ala Leu Gly Asp Ala Thr
65 70 75 80

Arg Ala Ile Glu Leu Asp Lys Lys Tyr Ile Lys Gly Tyr Tyr Arg Arg
85 90 95

Ala Ala Ser Asn Met Ala Leu Gly Lys Phe Arg Ala Ala Leu Arg Asp

